

**Supplemental Table S2.** Quantitative evaluation of the deviation from the consensus sequences derived from the protein alignment in Supplemental Figure S3.

	locus identifier	label for encoded protein	number of deviations from general CDA consensus <sup>1</sup>	number of deviations from plant CDA consensus <sup>1</sup>	number of insertions or deletions	Is this protein a functional CDA?
<i>Manihot esculenta</i>	cassava4.1_027753m	Mes1	0	1 <sup>2</sup>	0	likely
	cassava4.1_034385m	Mes2	0	0	0	yes
<i>Linum usitatissimum</i>	Lus10018355	Lus1	0	0	0	yes
	Lus10007654	Lus2	0	0	1	unsure
<i>Populus trichocarpa</i>	Potri.018G066400.1	Ptr1	0	0	0	yes
	Potri.006G150600.1	Ptr2	0	1	0	likely, because exchange at position 110 is conservative (Y to F)
<i>Medicago truncatula</i>	Medtr8g101570.1	Mtr1	0	1	0	likely, because G to S exchange at position 54, which is also observed in functional Gma1 and Gma2 (but here G to A)
	Medtr6g092660.1	Mtr2	0	5	0	unsure
<i>Phaseolus vulgaris</i>	Phvul.002G304000.1	Pvu1	0	1	0	likely, because conservative V to L exchange at position 33
	Phvul.004G170900.1	Pvu2	0	2	0	likely, because the same non-consensus exchanges at positions 70 and 73 are observed in functional Gma2 (however Gma2 is less active than Gma1 which has the consensus)
<i>Glycine max</i>	Glyma05g36320.1	Gma1	0	2 <sup>3</sup>	0	yes, experimentally confirmed
	Glyma07g15510.1	Gma2	0	4	0	yes, experimentally confirmed but less active than Gma1
	Glyma08g03280.1	Gma3	2	7	1	unlikely

<i>Malus domestica</i>	MDP0000736762	Mdo1	0	1	0	likely, because conservative L to F exchange at position 280 is present on both proteins of <i>Malus domestica</i>
	MDP0000568474	Mdo2	0	1	0	likely, because conservative L to F exchange at position 280 is present on both proteins of <i>Malus domestica</i>
<i>Brassica rapa</i>	Bra039004	Bra1	0	2	0	likely, because only conservative L to V exchange at position 260 and L to I exchange at position 278
	Bra024140	Bra2	0	2 <sup>2</sup>	0	likely, because only conservative V to L exchange at position 7. The second conservative A to S exchange at position 98 is also observed in other species <sup>2</sup>
	Bra024141	Bra3	2	12	3	unlikely
<i>Gossypium raimondii</i>	Gorai.004G284000.1	Gra1	0	0	0	yes
	Gorai.013G228000.1	Gra2	0	2	0	unsure
	Gorai.009G031100.1	Gra3	0	0	0	yes

<sup>1</sup> see Figure S1 for the deduction of the consensus

<sup>2</sup> This exchange (A to S at position 98 in Cru) is also observed in Mes1 and Bra2. The Cru protein is likely to be functional because it is the only well conserved CDA in *Capsella rubella*

<sup>3</sup> The soybean genome sequence contains a Y codon at position 164 of Gma1-CDA. Sequencing of the corresponding cDNA in this work revealed that there must be a sequence error in the genome sequence. The cDNAs code N at position 164 as found in the plant consensus for CDA. The amino acid sequence derived from the cDNA is shown in the alignment.